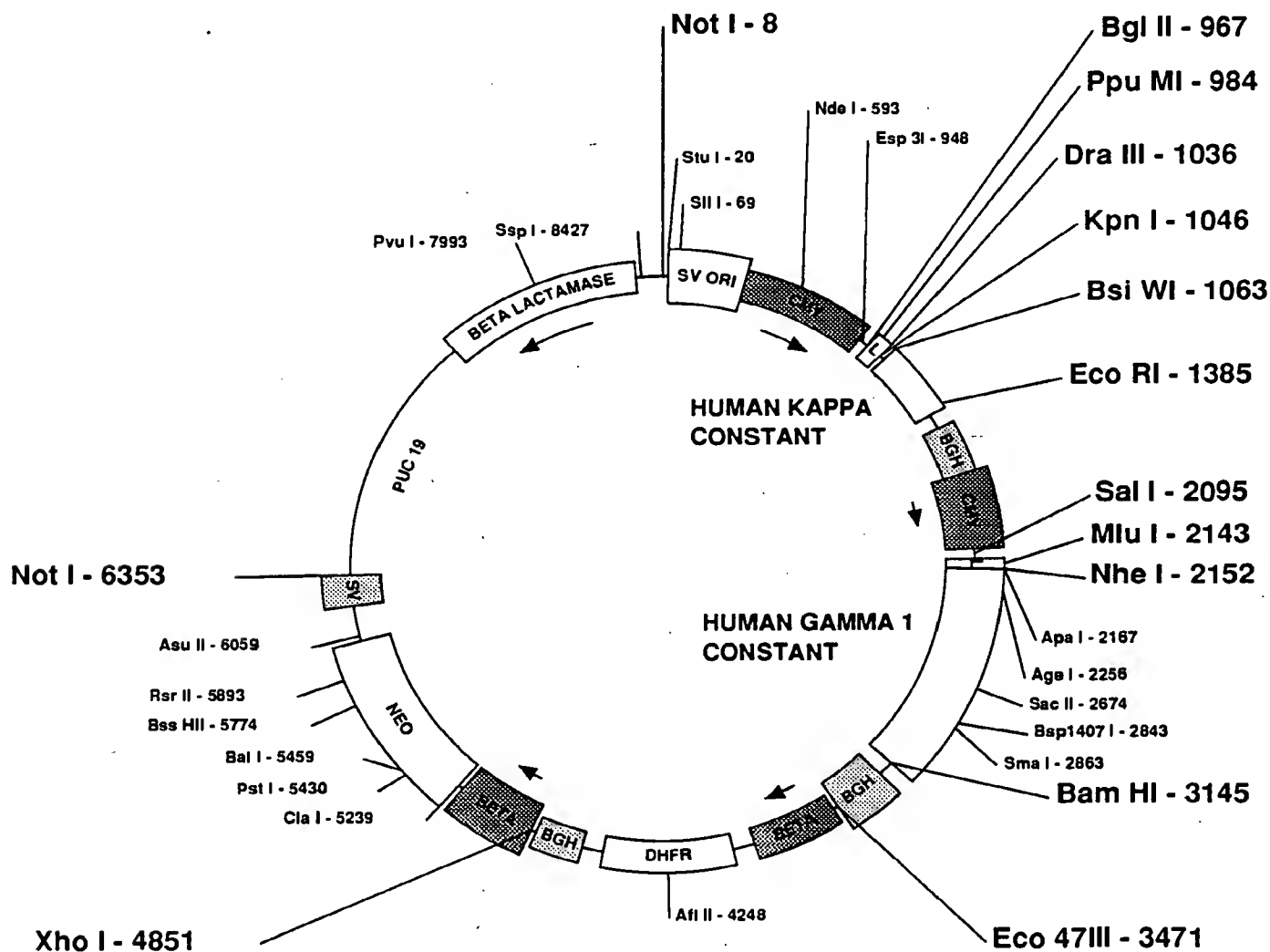


TCAE 8



8540 BP MAP BY MITCHELL REFF 11/8/92

L=Leader, CMV=Cytomegalovirus promoter
BETA=Mouse beta globin major promoter
BGH=Bovine growth hormone polyadenylation
SV=SV40 early polyadenylation
SV ORI=SV40 origin

Noncutters=AscI, AvrII, BspMII, Bst1107I
HindIII, I-PpoI, Maml, Muni, Nrul, PacI, Pml
Pml, RemI, SgrAI, SpeI, SrfI, Sse8387I, SwaI
XbaI, XcmI

^{linker #1 15bp}
GACGTCGCGG CCGCTCTAGG CCTCCAAAAA ^{SV40 origin = 332 bp} AGCCTCCTCA-CTACTTCTGG AATAGCTCAG 60
AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAT TAGTCAGCCA TGCATGGGGC 120
GGAGAATGGG CGGAAGTGGG CGGAGTTAGG GGCGGGATGG GCGGAGTTAG GGGCGGGACT 180
ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCCTGCTGG GGAGCCTGGG 240
GACTTTCCAC ACCTGGTTGC TGAATAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300
GGGGAGCCTG GGGACTTTCC ACACCCTAAC TGACACACAT TCCACAGAAAT ^{linker #2 = 13bp} TAATTCCTCT 360
^{347/8}
AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC 420
GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTT 480
ACGTCAATAA TGACGTATGT ^{CMV promoter-enhancer = 567 bp} TCCCAGTAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA 540
TGGGTGGACT ATTTACGGTA AACTGCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA 600
AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATTG TGCCAGTAC 660
ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC 720
ATGGTGATGC GGTTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA 780
TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA AAATCAACGG 840
GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA 900
CGGTGGGAGG TCTATATAAG CAGAGCTGGG ^{linker #3} TACGTGAACC GTCAGATCGC CTGGAGACGC 960
^{8-2 II}
CATCACAGAT ^{97/9} CTCTCACCAT GAGGGTCCCC GCTCAGCTCC ^{leader = 60bp} TGGGGCTCCT GCTGCTCTGG 1020
CTCCCAGGTG CACGATGTGA ^{107/108} TGGTACCAAG GTGGAAATCA ^{107/108} AACGTACGGT GGCTGCACCA 1080
^{107/108}
TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAAGTGC CTCTGTTGTG 1140
TGCCTGCTGA ATAACTTCTA TCCCAGAGAG GCCAAAGTAC AGTGGAAGGT GGATAACGCC 1200
CTCCAATCGG ^{human kappa constant 324 bp} GTAACCTCCA GGACAGTGTC ACAGAGCAGG ACAGCAAGGA CAGCACCTAC 1260
AGCCTCAGCA GCACCCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA AGTCTACGCC 1320
TGCGAAGTCA CCCATCAGGG CCTGAGCTCG CCCGTCACAA AGAGCTTCAA CAGGGGAGAG 1380
^{STOP}
^{RIGHT}
^{CHAIN} TGTGATTTC ^{EcoRI} AGATCCGTTA ^{linker #4 = 85 bp} ACGGTTACCA ACTACCTAGA CTGGATTCTG GACAACATGC 1440
^{138/7}
GGCCGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT 1500
GTTTGCCCCCT CCCCCGTGCC TTCCTTGACC CTGGAAGGTG CCACTCCAC TGTCCTTTCC 1560
^{BGH poly A = 231 bp}
TAATAAAATG AGGAAATTGC ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1620
GGGGTGGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1680

CGGGTGGGCT CTATGGAACC AGCTGGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG 1740
 ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT 1800
 TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT 1860
 GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCAGC GGGATTTCCT AGTCTCCACC 1920
 CCATTGACGT CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC 1980
 GTAACAACTC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2040
 TAAGCAGAGC TGGGTACGTC CTCACATTCA GTGATCAGCA CTGAACACAG ACCCGTCGAC 2100
 ATGGGTTGGA GCCTCATCTT GCTCTTCCTT GTCGCTGTG CTACGCGTGT CGCTAGCACC 2160
 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 2220
 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGGTGTC GTGGAATCA 2280
 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 2340
 TCCCTCAGCA GCGTGGTGAC CGTCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 2400
 AACGTGAATC ACAAGCCCAG CACACCAAG GTGGACAAGA AAGCAGAGCC CAAATCTTGT 2460
 GACAAAACTC ACACATGCCC ACCGTGCCCC GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 2520
 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 2580
 TGGGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 2640
 GGGGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 2700
 CGTGTGGTCA GCGTCTTCAC CGTCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 2760
 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 2820
 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 2880
 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 2940
 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 3000
 GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 3060
 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 3120
 CTCTCCCTGT CTCCGGGTAA ATGAGGATCC GTTAACGGTT ACCAACTACC TAGACTGGAT 3180
 TCGTGACAAC ATGGGCGCGT GATATCTACG TATGATCAGC CTCGACTGTG CCTTCTAGTT 3240
 GCCAGCCATC TGTTGTTTGC CCTCCCCCG TGCTTCTCTT GACCCTGGAA GGTGCCACTC 3300
 CCACTGTCCT TTCCTAATAA AATGAGGAAA TTGCATCGCA TTGTCTGAGT AGGTGTGATT 3360
 CTATTCTGGG GGGTGGGGTG GGGCAGGACA GCAAGGGGGA GGATTGGGAA GACAATAGCA 3420
 GGCATGCTGG GGATGCGGTG GGCTCTATGG AACCAGCTGG GGCTCGACAG CGCTGGATCT 3480

linker # 5 = 156 bp
 1762/3 1717/8
 CMV promoter-enhancer = 334 bp
 2061/2 2058/4
 leader = 51 bp
 MluI 2051/2 NheI
 -5 -4 -3 114 115
 2100 1 START heavy chain
 human gamma 1 constant
 993 bp = 330 AA + stop codon
 linker # 7 = 81 bp
 heavy chain 3144/5
 3225/6
 Bovine growth hormone polyadenylation region = 231 bp
 linker # 8 = 34 bp
 3456/7

CCCGATCCCC AGCTTTGCTT CTCAATTTCT TATTTGCATA ATGAGAAAAA AAGGAAAATT 3540
 3490/1
 AATTTTAACA CCAATTCAGT AGTTGATTGA GCAAATGCGT TGCCAAAAAG GATGCTTTAG 3600
 AGACAGTGT CTCTGCACAG ATAAGGACAA ACATTATTCA GAGGGAGTAC CCAGAGCTGA 3660
 Mouse Beta globin major promoter = 366bp
 GACTCCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCGAA 3720
 GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGAGAGG 3780
 GCAGGAGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCTCCTC ACATTTGCTT 3840
 CTGACATAGT TGTGTTGGGA GCTTGGATAG CTTGGACAGC TCAGGGCTGC GATTTTCGCGC 3900
 linker # 9 = 19bp 5' untranslated DHFR = 82bp
 385/7 3875/6 START DHFR
 CAAACTTGAC GGCAATCCTA GCGTGAAGGC TGGTAGGATT TTATCCCCGC TGCCATCATG 3960
 3157/8
 GTTCGACCAT TGAAGTGCAT CGTCGCCGTG TCCCAAAATA TGGGGATTGG CAAGAACGGA 4020
 GACCTACCCT GGCTCCGCT CAGGAACGAG TTCAAGTACT TCCAAAGAAT GACCACAACC 4080
 TCTTCAGTGG AAGGTAAACA GAATCTGGTG ATTATGGGTA GGAAAACCTG GTTCTCCATT 4140
 Mouse DHFR = 564bp = 187 aminoacids + stop codon
 CCTGAGAAGA ATCGACCTTT AAAGGACAGA ATTAATATAG TTCTCAGTAG AGAACTCAAA 4200
 GAACCACCAC GAGGAGCTCA TTTTCTTGCC AAAAGTTTGG ATGATGCCTT AAGACTTATT 4260
 GAACAACCGG AATTGGCAAG TAAAGTAGAC ATGGTTTGGGA TAGTCGGAGG CAGTTCTGTT 4320
 TACCAGGAAG CCATGAATCA ACCAGGCCAC CTTAGACTCT TTGTGACAAG GATCATGCAG 4380
 GAATTTGAAA GTGACACGTT TTTCCAGAA ATTGATTTGG GGAAATATAA ACTTCTCCCA 4440
 GAATACCCAG GCGTCCTCTC TGAGGTCCAG GAGGAAAAAG GCATCAAGTA TAAGTTTGAA 4500
 STOP DHFR 452/2
 GTCTACGAGA AGAAAGACATA ACAGGAAGAT GCTTTCAAGT TCTCTGCTCC CCTCCTAAAG 4560
 3' untranslated DHFR = 82bp linker # 10 = 10bp
 CTATGCATTT TTATAAGACC ATGGGACTTT TGCTGGCTTT AGATCAGCCT CGACTGTGCC 4620
 4603/4 4631/4
 TTCTAGTTGC CAGCCATCTG TTGTTTGCCC CTCCCCCGTG CCTTCCTTGA CCCTGGAAGG 4680
 Bovine growth hormone polyadenylation region = 231bp
 TGCCACTCCC ACTGTCCTTT CCTAATAAAA TGAGGAAATT GCATCGCATT GTCTGAGTAG 4740
 GTGTCATTCT ATTCTGGGGG GTGGGGTGGG GCAGGACAGC AAGGGGGAGG ATTGGGAAGA 4800
 CAATAGCAGG CATGCTGGGG ATGCGGTGGG CTCTATGGAA CCAGCTGGGG CTCGAGCTAC 4860
 linker # 11 = 17bp
 4841/5
 TAGCTTTGCT TCTCAATTC TTATTTGCAT AATGAGAAAA AAAGGAAAAT TAATTTTAAC 4920
 4861/2
 ACCAATTCAG TAGTTGATTG AGCAAATGCG TTGCCAAAAA GGATGCTTTA GAGACAGTGT 4980
 Mouse beta globin major promoter = 366bp
 TCTCTGCACA GATAAGGACA AACATTATTC AGAGGGAGTA CCCAGAGCTG AGACTCCTAA 5040
 GCCAGTGAGT GGCACAGCAT TCTAGGGAGA AATATGCTTG TCATCACCGA AGCCTGATTC 5100
 CGTAGAGCCA CACCTTGGTA AGGGCCAATC TGCTCACACA GGATAGAGAG GGCAGGAGCC 5160
 AGGGCAGAGC ATATAAGGTG AGGTAGGATC AGTTGCTCCT CACATTTGCT TCTGACATAG 5220
 linker # 12 = 21bp START NEO
 TTGTGTGGG AGCTTGGATC GATCCTCTAT GTTGAACAA GATGGATTGC ACGCAGGTTC 5280
 5227/8 5248/9

TCCGGCCGCT TGGGTGGAGA GGCTATTCGG CTATGACTGG GCACAACAGA CAATCGGCTG 5340
CTCTGATGCC GCCGTGTTCC GGCTGTCAGC GCAGGGGCGC CCGGTTCTTT TTGTCAAGAC 5400
CGACCTGTCC *Neomycin phosphotransferase*
GGTGCCCTGA ATGAAGTGA GGACGAGGCA GCGCGGCTAT CGTGGCTGGC 5460
795 bp = 264 amino acids + stop codon
CACGACGGGC GTTCCTTGCG CAGCTGTGCT CGACGTTGTC ACTGAAGCGG GAAGGGACTG 5520
GCTGCTATTG GGCGAAGTGC CGGGGCAGGA TCTCCTGTCA TCTCACCTTG CTCCTGCCGA 5580
GAAAGTATCC ATCATGGCTG ATGCAATGCG GCGGCTGCAT ACGCTTGATC CGGCTACCTG 5640
CCCATTCGAC CACCAAGCGA AACATCGCAT CGAGCGAGCA CGTACTCGGA TGGAAGCCGG 5700
TCTTGTCGAT CAGGATGATC TGGACGAAGA GCATCAGGGG CTCGCGCCAG CCGAACTGTT 5760
CGCCAGGCTC AAGGCGCGCA TGCCCGACGG CGAGGATCTC GTCGTGACCC ATGGCGATGC 5820
CTGCTTGCCG AATATCATGG TGGAAAATGG CCGCTTTTCT GGATTCATCG ACTGTGGCCG 5880
GCTGGGTGTG GCGGACCGCT ATCAGGACAT AGCGTTGGCT ACCCGTGATA TTGCTGAAGA 5940
GCTTGGCGGC GAATGGGCTG ACCGCTTCCT CGTGCTTTAC GGTATCGCCG CTCCCGATTC 6000
GCAGCGCATC GCCTTCTATC GCCTTCTTGA *STOP NEO* CGAGTTCTTC *60 43 4* TCGCGGGAC TCTGGGGTTC 6060
GAAATGACCG ACCAAGCGAC GCCCAACCTG CCATCAGCAG ATTTCGATTC CACCGCCGCC 6120
3' untranslated NEO = 173 bp
TTCTATGAAA GGTGGGGCTT CGGAATCGTT TTCCGGGACG CCGGCTGGAT GATCCTCCAG 6180
CGCGGGGATC TCATGCTGGA GTTCTTCGCC CACCCCAACT *6216 7* TGTATTATGC AGCTTATAAT 6240
GGTTACAAAT AAAGCAATAG CATCACAAAT TTCACAAATA AAGCATTTTT TTTACTGCAT 6300
SV40 poly A early = 133 bp
TCTAGTTGTG GTTTGTCCAA ACTCATCAAT CTATCTTATC ATGTCTGGAT *linker = 13 = 19 bp* CGCGGCCGCG 6360
6349 50
ATCCCGTGA *6349 19* GAGCTTGGCG TAATCATGGT CATAGCTGTT TCCTGTGTGA AATTGTTATC 6420
CGCTCACAAAT TCCACACAAC ATACGAGCCG GAAGCATAAA GTGTAAAGCC TGGGGTGCCT 6480
AATGAGTGAG CTAATCACA TTAATTGCGT TGCCTCACT GCCCGCTTTC CAGTCGGGAA 6540
ACCTGTCGTG CCAGCTGCAT TAATGAATCG GCCAACGCGC GGGGAGAGGC GGTTTGCGTA 6600
PUC 19
TTGGGCGCTC TTCCGCTTCC TCGCTCACTG ACTCGCTGCG CTCGGTCGTT CGGCTGCGGC 6660
GAGCGGTATC AGCTCACTCA AAGGCGGTAA TACGGTTATC CACAGAATCA GGGGATAACG 6720
CAGGAAAGAA CATGTGAGCA AAAGGCCAGC AAAAGGCCAG GAACCGTAAA AAGGCCGCGT 6780
6792 = bacterial origin of replication
TGCTGGCGTT *TTTCCATAGG* CTCCGCCCCC CTGACGAGCA TCACAAAAAT CGACGCTCAA 6840
GTCAGAGGTG GCGAAACCCG ACAGGACTAT AAAGATACCA GGCCTTTCCC CCTGGAAGCT 6900
CCCTCGTGCG CTCTCCTGTT CCGACCCTGC CGCTTACCGG ATACCTGTCC GCCTTTCTCC 6960
CTTCGGGAAG CGTGGCGCTT TCTCAATGCT CACGCTGTAG GTATCTCAGT TCGGTGTAGG 7020
TCGTTGCTC CAAGCTGGGC TGTGTGCACG AACCCCCGT TCAGCCCGAC CGCTGCGCCT 7080

TATCCGGTAA	CTATCGTCTT	GAGTCCAACC	CGGTAAGACA	CGACTTATCG	CCACTGGCAG	7140
CAGCCACTGG	TAACAGGATT	AGCAGAGCGA	GGTATGTAGG	CGGTGCTACA	GAGTTCCTGA	7200
AGTGGTGGCC	TAACTACGGC	TACACTAGAA	GGACAGTATT	TGGTATCTGC	GCTCTGCTGA	7260
AGCCAGTTAC	CTTCGGAAAA	AGAGTTGGTA	GCTCTTGATC	CGGCAAAACAA	ACCACCGCTG	7320
GTAGCGGTGG	TTTTTTTGT	TGCAAGCAGC	AGATTACGCG	CAGAAAAAAA	GGATCTCAAG	7380
AAGATCCTTT	GATCTTTTCT	ACGGGGTCTG	ACGCTCAGTG	GAACGAAAAC	TCACGTTAAG	7440
GGATTTTGGT	CATGAGATTA	TCAAAAAGGA	TCTTCACCTA	GATCCTTTTA	AATTAAAAAT	7500
GAAGTTTAA	ATCAATCTAA	AGTATATATG	AGTAAACTTG	GTCTGACAGT	TACCAATGCT	7560
TAATCAGTGA	GGCACCTATC	TCAGCGATCT	GTCTATTTTCG	TTCATCCATA	GTTGCCTGAC	7620
TCCCCGTCGT	GTAGATAACT	ACGATACGGG	AGGGCTTACC	ATCTGGCCCC	AGTGCTGCAA	7680
TGATACCGCG	AGACCCACGC	TCACCGGCTC	CAGATTTATC	AGCAATAAAC	CAGCCAGCCG	7740
GAAGGGCCGA	GCGCAGAAAGT	GGTCCTGCAA	CTTTATCCGC	CTCCATCCAG	TCTATTAATT	7800
GTTGCCGGGA	AGCTAGAGTA	AGTAGTTCGC	CAGTTAATAG	TTTGCGCAAC	GTTGTTGCCA	7860
TTGCTACAGG	CATCGTGGTG	TCACGCTCGT	CGTTTGGTAT	GGCTTCATTC	AGCTCCGGTT	7920
CCCAACGATC	AAGGCGAGTT	ACATGATCCC	CCATGTTGTG	CAAAAAAGCG	GTTAGCTCCT	7980
TCGGTCTCC	GATCGTTGTC	AGAAGTAAGT	TGGCCGCACT	GTTATCACTC	ATGGTTATGG	8040
CAGCACTGCA	TAATTCTCTT	ACTGTCATGC	CATCCGTAAG	ATGCTTTTCT	GTGACTGGTG	8100
AGTACTCAAC	CAAGTCATTC	TGAGAATAGT	GTATGCGGCG	ACCGAGTTGC	TCTTGCCCCG	8160
CGTCAATACG	GGATAATACC	GCGCCACATA	GCAGAACTTT	AAAAGTGCTC	ATCATTTGAA	8220
AACGTTCTTC	GGGGCGAAAA	CTCTCAAGGA	TCTTACCGCT	GTTGAGATCC	AGTTCGATGT	8280
AACCCACTCG	TGCACCCAAC	TGATCTTCAG	CATCTTTTAC	TTTCACCAGC	GTTTCTGGGT	8340
GAGCAAAAAC	AGGAAGGCAA	AATGCCGCAA	AAAAGGGAAT	AAGGGCGACA	CGGAAATGTT	8400
GAATACTCAT	ACTCTTCCTT	TTTCAATATT	ATTGAAGCAT	TTATCAGGGT	TATTGTCTCA	8460
TGAGCGGATA	CATATTTGAA	TGTATTTAGA	AAAATAAACA	AATAGGGGTT	CCGCGCACAT	8520
TTCCCCGAAA	AGTGCCACCT					

Linker # 1 = 15 bp
 GACGTCGCGG CCGCTCTAGG CCTCCAAAAA AGCCTCCTCA CTA CTCTCTGG AATAGCTCAG 60
 AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAAT TAGTCAGCCA TGCATGGGGC 120
 GGAGAATGGG CGGAACTGGG CGGAGTTAGG GCGGGGATGG GCGGAGTTAG GGGCGGGACT 180
 ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCCTGCTGG GGAGCCTGGG 240
 GACTTTCCAC ACCTGGTTGC TGACTAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300
 GGGGAGCCTG GGGACTTTCC ACACCCTAAC TGACACACAT TCCACAGAAT TAATTCCCCCT 360
 AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCGCG 420
 GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG 480
 ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA 540
 TGGGTGGACT ATTTACGTA AACTGCCAC TTGGCAGTAC ATCAAGTGA TCATATGCCA 600
 AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCC CCTGGCATTG TGCCAGTAC 660
 ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC 720
 ATGGTGATGC GGTTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA 780
 TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA AAATCAACGG 840
 GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA 900
 CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC 960
 CATCACAGAT CTCTCACTAT GATTTCAG GTGCAGATTA TCAGCTTCCT GCTAATCAGT 1020
 GCTTCAGTCA TAATGTCCAG AGGACAAATT GTTCTCTCCC AGTCTCCAGC AATCCTGTCT 1080
 GCATCTCCAG GGGAGAAGGT CACAATGACT TGCAGGGCCA GCTCAAGTGT AAGTTACATC 1140
 CACTGGTTCC AGCAGAAGCC AGGATCCTCC CCCAAACCCCT GGATTATATGC CACATCCAAC 1200
 CTGGCTTCTG GAGTCCCTGT TCGCTTCAGT GGCAGTGGGT CTGGGACTTC TTA CTCTCTC 1260
 ACAATCAGCA GAGTGGAGGC TGAAGATGCT GCCACTTATT ACTGCCAGCA GTGGACTAGT 1320
 AACCCACCCA CGTTCGGAGG GGGGACCAAG CTGGAAATCA AACGTACGGT GGCTGCACCA 1380
 TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAAGTGC CTCTGTTGTG 1440
 TGCCTGCTGA ATA ACTTCTA TCCAGAGAG GCCAAAGTAC AGTGGAAAGGT GGATAACGCC 1500
 CTCCAATCGG GTA ACTCCA GGAGAGTGT ACAGAGCAGG ACAGCAAGGA CAGCACCTAC 1560
 AGCCTCAGCA GCACCCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA AGTCTACGCC 1620
 TGCGAAGTCA CCCATCAGGG CCTGAGCTCG CCCGTCACAA AGAGCTTCAA CAGGGGAGAG 1680

SV40 origin = 332 bp
 linker # 2 = 13 bp
 CMV promoter-enhancer = 567 bp
 Bgl II
 linker # 3
 natural leader = 66 bp
 light chain variable region 318 bp 106 AA
 BsiwI
 human kappa constant = 324 bp = 107 AA + stop codon

STOP
 linker #4 = 81 bp
 TGTTGAATTC AGATCCGTTA ACGGTTACCA ACTACCTAGA CTGGATTTCGT GACAACATGC 1740
 1646 7
 GGCCGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT 1800
 1771 2
 GTTTGCCCTT CCCCCGTGCC TTCCTTGACC CTGGAAGGTG CCACTCCAC TGTCCTTTCC 1860
 TAATAAAATG AGGAAATTGC ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1920
 Bovine growth hormone polyadenylation region = 231 bp
 GGGGTGGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1980
 linker #5 = 15 bp
 GCGGTGGGCT CTATGGAACC AGCTGGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG 2040
 2002 3 2017 8
 ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT 2100
 TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT 2160
 CMV promoter-enhancer = 334 bp
 GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCAGC GGGATTTCCA AGTCTCCACC 2220
 CCATTGACGT CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC 2280
 GTAACAATC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2340
 7 bp
 TAAGCAGAGC TGGGTACGTC CTCACATTCA GTGATCAGCA CTGAACACAG ACCCGTCGAC 2400
 2351 2 2358 9
 start heavy chain 2400
 ATGGGTTGGA GCCTCATCTT GCTCTTCCTT GTCGCTGTTG CTACGGCTGT CCTGTCCAG 2460
 Synthetic + natural leader MluI
 -5 -4 -3 -2 -1 +1
 GTACAATGC AGCAGCCTGG GGCTGAGCTG GTGAAGCCTG GGGCTCAGT GAAGATGTCC 2520
 TGCAAGGCTT CTGGCTACAC ATTTACCAGT TACAATATGC ACTGGGTAAA ACAGACACCT 2580
 heavy chain variable = 363 bp = 121 A.A.
 GGTGCGGGCC TGGAAATGGAT TGGAGCTATT TATCCCGGAA ATGGTGATAC TTCCTACAAT 2640
 CAGAAGTTCA AAGGCAAGGC CACATTGACT GCAGACAAAT CCTCCAGCAC AGCCTACATG 2700
 CAGCTCAGCA GCCTGACATC TGAGGACTCT GCGGTCTATT ACTGTGCAAG ATCGACTTAC 2760
 TACGGCGGTG ACTGGTACTT CAATGTCTGG GGCGCAGGGA CCACGGTCAC CGTCTCTGCA 2820
 NheI 2820 1
 GCTAGCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCTT CCTCCAAGAG CACCTCTGGG 2880
 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG 2940
 human gamma 1 constant = 993 bp
 TGGAATCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCTT ACAGTCCTCA 3000
 330 A.A. + stop codon
 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC 3060
 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGCAGAGCCC 3120
 AAATCTTGTG ACAAACCTCA CACATGCCCA CCGTGCCCAG CACCTGAACT CCTGGGGGGA 3180
 CCGTCAGTCT TCCTCTTCCC CCAAAAACCC AAGGACACCC TCATGATCTC CCGGACCCCT 3240
 GAGGTCACAT GCGTGGTGGT GGACGTGAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG 3300
 TACGTGGACG GCGTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGAGGA GCAGTACAAC 3360
 AGCACGTACC GTGTGGTCAG CGTCCTCACC GTCCTGCACC AGGACTGGCT GAATGGCAAG 3420
 GAGTACAAGT GCAAGGTCTC CAACAAAGCC CTCCAGCCCC CCATCGAGAA AACCATCTCC 3480

AAAGCCAAAG	GGCAGCCCCG	AGAACCACAG	GTGTACACCC	TGCCCCCATC	CCGGGATGAG	3540
CTGACCAAGA	ACCAGGTCAG	CCTGACCTGC	CTGGTCAAAG	GCTTCTATCC	CAGCGACATC	3600
GCCGTGGAGT	GGGAGAGCAA	TGGGCAGCCG	GAGAACAAC	ACAAGACCAC	GCCTCCCGTG	3660
CTGGACTCCG	ACGGCTCCTT	CTTCCTCTAC	AGCAAGCTCA	CCGTGGACAA	GAGCAGGTGG	3720
CAGCAGGGGA	ACGTCTTCTC	ATGCTCCGTG	ATGCATGAGG	CTCTGCACAA	CCACTACACG	3780
CAGAAGAGCC	TCTCCCTGTC	TCCGGGTAA	TGAGGATCCG	TTAACGGTTA	CCAACTACCT	3840
AGACTGGATT	CGTGACAACA	TGCGGCCGTG	ATATCTACGT	ATGATCAGCC	TCGACTGTGC	3900
CTTCTAGTTG	CCAGCCATCT	GTTGTTTGCC	CCTCCCCCGT	GCCTTCCTTG	ACCTGGAAG	3960
GTGCCACTCC	CACTGTCCTT	TCCTAATAAA	ATGAGGAAAT	TGCATCGCAT	TGTCTGAGTA	4020
GGTGTCAATC	TATTCTGGGG	GGTGGGGTGG	GGCAGGACAG	CAAGGGGGAG	GATTGGGAAG	4080
ACAATAGCAG	GCATGCTGGG	GATGCGGTGG	GCTCTATGGA	ACCAGCTGGG	GCTCGACAGC	4140
GCTGGATCTC	CCGATCCCCA	GCTTTGCTTC	TCAATTTCTT	ATTTCGATAA	TGAGAAAAAA	4200
AGGAAAATTA	ATTTTAACAC	CAATTCAGTA	GTTGATTGAG	CAAATGCGTT	GCCAAAAAGG	4260
ATGCTTTAGA	GACAGTGTTC	TGTGCACAGA	TAAGGACAAA	CATTATTCAG	AGGGAGTACC	4320
CAGAGCTGAG	ACTCCTAAGC	CAGTGAGTGG	CACAGCATTG	TAGGGAGAAA	TATGCTTGTC	4380
ATCACCGAAG	CCTGATTCCG	TAGAGCCACA	CCTTGGAAG	GGCCAATCTG	CTCACACAGG	4440
ATAGAGAGGG	CAGGAGCCAG	GGCAGAGCAT	ATAAGGTGAG	GTAGGATCAG	TTGCTCCTCA	4500
CATTTGCTTC	TGACATAGTT	GTGTGGGAG	CTTGGATAGC	TTGGACAGCT	CAGGGCTGCG	4560
ATTTGCGGCC	AAACTTGACG	GCAATCCTAG	CGTGAAGGCT	GGTAGGATTT	TATCCCCGCT	4620
GCCATCATGG	TTGACACATT	GAAGTGCATC	GTCGCCGTGT	CCCAAATAT	GGGGATTGGC	4680
AAGAACGGAG	ACCTACCCTG	GCCTCCGCTC	AGGAACGAGT	TCAAGTACTT	CCAAAGAATG	4740
ACCACAACCT	CTTCAGTTGA	AGGTAAACAG	AATCTGGTGA	TTATGGGTAG	GAAAACCTGG	4800
TTCTCCATTC	CTGAGAAGAA	TCGACCTTTA	AAGGACAGAA	TTAATATAGT	TCTCAGTAGA	4860
GAAGTCAAAG	AACCACCACG	AGGAGCTCAT	TTTCTTGCCA	AAAGTTTGGA	TGATGCCTTA	4920
AGACTTATTG	AACAACCGGA	ATTGGCAAGT	AAAGTAGACA	TGGTTTGGAT	AGTCGGAGGC	4980
AGTTCTGTTT	ACCAGGAAGC	CATGAATCAA	CCAGGCCACC	TTAGACTCTT	TGTGACAAGG	5040
ATCATGCAGG	AATTTGAAAG	TGACACGTTT	TTCCAGAAA	TTGATTTGGG	GAAATATAAA	5100
CTTCTCCCAG	AATACCCAGG	CGTCCTCTCT	GAGGTCCAGG	AGGAAAAAGG	CATCAAGTAT	5160
AAGTTTGAAG	TCTACGAGAA	GAAAGACTAA	CAGGAAGATG	CTTTCAAGTT	CTCTGCTCCC	5220
CTCCTAAAGC	TATGCATTTT	TATAAGACCA	TGGGACTTTT	GCTGGCTTTA	GATCAGCCTC	5280

Bovine growth hormone polyadenylation region = 231 bp
 mouse Beta globin major promoter = 366 bp
 DHFR = 564 bp = 187 amino acid + stop codon
 5' untranslated DHFR = 82 bp
 3' untranslated DHFR = 82 bp
 linker # 1 = 19 bp
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 linker #

GACTGTGCCT TCTAGTTGCC AGCCATCTGT TGTTCGCCCC TCCCCGTGC CTTCCTTGAC 5340
 CCTGGAAGGT *Bovine growth hormone polyadenylation = 231 bp* GCCACTCCCA CTGTCCTTTC CTAATAAAAT GAGGAAATTG CATCGCATTG 5400
 TCTGAGTAGG TGTCAATTCTA TTCTGGGGGG TGGGGTGGGG CAGGACAGCA AGGGGGAGGA 5460
 TTGGGAAGAC AATAGCAGGC ATGCTGGGGA TCGGTGGGC TCTATGGAAC *linker # 11 = 17 bp* CAGCTGGGGC 5520
 TCGAGCTACT *5530* AGCTTTGCTT CTCAATTTCT TATTTGCATA ATGAGAAAAA AAGGAAAATT 5580
 AATTTTAACA CCAATTCAGT AGTTGATTGA GCAAATGCGT TGCCAAAAAG GATGCTTTAG 5640
 AGACAGTGTT *Mouse beta globin major promoter = 366 bp* CTCTGCACAG ATAAGGACAA ACATTATTCA GAGGGAGTAC CCACAGCTGA 5700
 GACTCCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCGAA 5760
 GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGAGAGG 5820
 GCAGGAGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCTCCTC ACATTTGCTT 5880
 CTGACATAGT *linker # 12 = 21 bp* TGTGTTGGGA GCTTGGATCG ATCCTCTATG *start neo* GTTGAACAAG ATGGATTGCA 5940
 CGCAGGTTCT *5896* CCGGCCGCTT GGGTGGAGAG GCTATTCGGC TATGACTGGG CACAACAGAC 6000
 AATCGGCTGC TCTGATGCCG CCGTGTTCCG GCTGTCAGCG CAGGGGCGCC CGGTTCTTTT 6060
 TGTCAAGACC *Neomycin phosphotransferase = 795 bp = 264 AA + stop codon* GACCTGTCCG GTGCCCTGAA TGAAGTGCAG GACGAGGCAG CGCGGCTATC 6120
 GTGGCTGGCC ACGACGGGCG TTCCTTGCGC AGCTGTGCTC GACGTTGTCA CTGAAGCGGG 6180
 AAGGGACTGG CTGCTATTGG GCGAAGTGCC GGGGCAGGAT CTCCTGTGAT CTCACCTTGC 6240
 TCCTGCCGAG AAAGTATCCA TCATGGCTGA TGCAATGCGG CGGCTGCATA CGCTTGATCC 6300
 GGCTACCTGC CCATTGACAC ACCAAGCGAA ACATCGCATC GAGCGAGCAC GTACTCGGAT 6360
 GGAAGCCGGT CTTGTGATC AGGATGATCT GGACGAAGAG CATCAGGGGC TCGCGCCAGC 6420
 CGAACTGTTT GCCAGGCTCA AGGCGCGCAT GCGCGACGGC GAGGATCTCG TCGTGACCCA 6480
 TGGCGATGCC TGCTTGCCGA ATATCATGGT GGAAATGGC CGCTTTTCTG GATTCATCGA 6540
 CTGTGGCCGG CTGGGTGTGG CGGACCGCTA TCAGGACATA GCGTTGGCTA CCCGTGATAT 6600
 TGCTGAAGAG CTTGGCGGCG AATGGGCTGA CCGCTTCCTC GTGCTTTACG GATCGCCGC 6660
 TCCCGATTCT CAGCGCATCG CCTTCTATCG CCTTCTTGAC GAGTTCTTCT *STOP NEO* GAGCGGGACT 6720
 CTGGGGTTCT AAATGACCGA CCAAGCGACG CCAACCTGC CATCACGAGA TTTCGATTCC 6780
 ACCGCCGCTT TCTATGAAAG GTTGGGCTTC GGAATCGTTT TCCGGGACGC CGGCTGGATG 6840
 ATCCTCCAGC GCGGGGATCT CATGCTGGAG TTCTTCGCCC ACCCAACTT GTTTATTGCA 6900
 GCTTATAATG GTTACAAATA AAGCAATAGC ATCACAATTC TCACAAATAA AGCATTTTTT 6960
 TCACTGCATT CTAGTTGTGG TTTGTCCAAA CTCATCAATC TATCTTATCA TGTCTGGATC *SV40 early polyadenylation region = 133 bp* 7020
 GCGGCCGCGA TCCCGTGGAG AGCTTGGCGT AATCATGGTC ATAGCTGTTT CCTGTGTGAA *linker # 13 = 19 bp* 7080
7037 *Puc 19*

07 978891

Puc 19

ATTGTTATCC	GCTCACAATT	CCACACAACA	TACGAGCCGG	AAGCATAAAG	TGTAAAGCCT	7140
GGGGTGCTTA	ATGAGTGAGC	TAACCTACAT	TAATTGCGTT	GCGCTCACTG	CCCGCTTTCC	7200
AGTCGGGAAA	CCTGTCGTGC	CAGCTGCATT	AATGAATCGG	CCAACGCGCG	GGGAGAGGCG	7260
GTTTGCGTAT	TGGGCGCTCT	TCCGCTTCCT	CGCTCACTGA	CTCGCTGCGC	TGGTTCGTTC	7320
GGCTGCGGCG	AGCGGTATCA	GCTCACTCAA	AGGCGGTAAT	ACGGTTATCC	ACAGAATCAG	7380
GGGATAACGC	AGGAAAGAAC	ATGTGAGCAA	AAGGCCAGCA	AAAGGCCAGG	AACCGTAAAA	7440
AGGCCGCGTT	GCTGGCGTTT	TTCATAGGC	TCCGCCCCCG	TGACGAGCAT	CACAAAAATC	7500
GACGCTCAAG	TCAGAGGTGG	CGAAACCCGA	CAGGACTATA	AAGATACCAG	GCGTTTCCCC	7560
CTGGAAGCTC	CCTCGTGCGC	TCTCCTGTTC	CGACCCTGCC	GCTTACCGGA	TACCTGTCCG	7620
CCTTTCTCCC	TTCGGGAAGC	GTGGCGCTTT	CTCAATGCTC	ACGCTGTAGG	TATCTCAGTT	7680
CGGTGTAGGT	CGTTCGCTCC	AAGCTGGGCT	GTGTGCACGA	ACCCCCCGTT	CAGCCCGACC	7740
GCTGCGCCTT	ATCCGGTAAC	TATCGTCTTG	AGTCCAACCC	GGTAAGACAC	GACTTATCGC	7800
CACTGGCAGC	AGCCACTGGT	AACAGGATTA	GCAGAGCGAG	GTATGTAGGC	GGTGCTACAG	7860
AGTTCTTGAA	GTGGTGGCCT	AACTACGGCT	ACACTAGAAG	GACAGTATTT	GGTATCTGCG	7920
CTCTGCTGAA	GCCAGTTACC	TTCGGAAAAA	GAGTTGGTAG	CTCTTGATCC	GGCAAAACAA	7980
CCACCGCTGG	TAGCGGTGGT	TTTTTTGTTT	GCAAGCAGCA	GATTACGCGC	AGAAAAAAG	8040
GATCTCAAGA	AGATCCTTTG	ATCTTTTCTA	CGGGGTCTGA	CGCTCAGTGG	AACGAAAACT	8100
CACGTTAAGG	GATTTTGGTC	ATGAGATTAT	CAAAAAGGAT	CTTCACCTAG	ATCCTTTTAA	8160
ATTAAAAATG	AAGTTTTTAA	TCAATCTAAA	GTATATATGA	GTAAACTTGG	TCTGACAGTT	8220
APCAATGCTT	AATCAGTGAG	GCACCTATCT	CAGCGATCTG	TCTATTTCTG	TCATCCATAG	8280
TTGCTGACT	CCCCGTCGTG	TAGATAACTA	CGATACGGGA	GGGCTTACCA	TCTGGCCCCA	8340
GTGCTGCAAT	GATACCGCGA	GACCCACGCT	CACCGGCTCC	AGATTTATCA	GCAATAAACC	8400
AGCCAGCCGG	AAGGGCCGAG	CGCAGAAGTG	GTCCTGCAAC	TTTATCCGCC	TCCATCCAGT	8460
CTATTAATTG	TTGCCGGGAA	GCTAGAGTAA	GTAGTTCGCC	AGTTAATAGT	TTGCGCAACG	8520
TTGTTGCCAT	TGCTACAGGC	ATCGTGGTGT	CACGCTCGTC	GTTTGGTATG	GCTTCATTCA	8580
GCTCCGGTTC	CCAACGATCA	AGGCGAGTTA	CATGATCCCC	CATGTTGTGC	AAAAAAGCGG	8640
TTAGCTCCTT	CGGTCTCCG	ATCGTTGTCA	GAAGTAAGTT	GGCCGAGTG	TTATCACTCA	8700
TGGTTATGGC	AGCACTGCAT	AATTCTCTTA	CTGTCATGCC	ATCCGTAAGA	TGCTTTTCTG	8760
TGACTGGTGA	GTAACAACC	AAGTCATTCT	GAGAATAGTG	TATGCGGCGA	CCGAGTTGCT	8820
CTTGCCCGGC	GTCAATACGG	GATAATACCG	CGCCACATAG	CAGAACTTTA	AAAGTGCTCA	8880

7461 = bacterial origin of replication

8219 = stop Beta lactamase

Beta lactamase = 861bp = 286 A.A + stop codon

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TCATTGGAAA	ACGTTCTTCG	GGGCGAAAAC	TCTCAAGGAT	CTTACCGCTG	TTGAGATCCA	8940
GTTTCGATGTA	ACCCACTCGT	GCACCCAACT	GATCTTCAGC	ATCTTTTACT	TTCACCAGCG	9000
TTTCTGGGTG	AGCAAAAACA	GGAAGGCAAA	ATGCCGCAAA	AAAGGGAATA	AGGGCGACAC	9060
GGAAATGTTG	AATACTCATA	CTCTTCCTTT	TTCAATATTA	TTGAAGCATT	TATCAGGGTT	9120
ATTGTCTCAT	GAGCGGATAC	ATATTGAAT	GTATTTAGAA	AAATAAACAA	ATAGGGGTTT	9180
CGCGCACATT	TCCCCGAAAA	GTGCCACCT				

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mLght

FIGURE 4

5

Leader

10

Frame 1

Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser Val

ATG GAT TTT CAG GTG CAG ATT ATC AGC TTC CTG CTA ATC AGT GCT TCA GTC

987 996 1005 1014 1023

15

-5 -1 +1 FR1 10

Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser

ATA ATG TCC AGA GGA CAA ATT GTT CTC TCC CAG TCT CCA GCA ATC CTG TCT GCA TCT

1038 1047 1056 1065 1074 1083

20

20 23 24 CDR1 27/ 29 30 34

Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile His

CCA GGG GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC TCA AGT GTA AGT TAC ATC CAC

1095 1104 1113 1122 1131 1140

25

35 FR2 40 45 49 50 CDR2

Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn

TGG TTC CAG CAG AAG CCA GGA TCC TCC CCC AAA CCC TGG ATT TAT GCC ACA TCC AAC

1152 1161 1170 1179 1188 1197

30

55 56 57 60 FR3 65 70

Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser

CTG GCT TCT GGA GTC CCT GTT CGC TTC AGT GGC AGT GGG TCT GGG ACT TCT TAC TCT

1209 1218 1227 1236 1245 1254

35

75 80 85 88 89 90

Leu Thr Ile Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp

CTC ACA ATC AGC AGA GTG GAG GCT GAA GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG

1266 1275 1284 1293 1302 1311

40

CDR3 95 97 98 100 FR4 105 107

Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

ACT AGT AAC CCA CCC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATC AAA

1323 1332 1341 1350 1359

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mHvy

FIGURE 5

5

Leader

10

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15

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45

Frame 1	-19				-15					-10					-5				
	Met	Gly	Trp	Ser	Leu	Ile	Leu	Leu	Phe	Leu	Val	Ala	Val	Ala	Thr	Arg	Val		
	ATG	GGT	TGG	AGC	CTC	ATC	TTG	CTC	TTC	CTT	GTC	GCT	GTT	GCT	ACG	CGT	GTC		
			2409			2418			2427			2436			2445				
	-1	+1			FR1					10					15				
	Leu	Ser	Gln	Val	Gln	Leu	Gln	Pro	Gly	Ala	Glu	Leu	Val	Lys	Pro	Gly	Ala	Ser	
	CTG	TCC	CAG	GTA	CAA	CTG	CAG	CAG	CCT	GGG	GCT	GAG	CTG	GTG	AAG	CCT	GGG	GCC	TCA
		2460			2469			2478			2487			2496			2505		
		20				25					30	31		CDR1		35	36		
	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	Asn	Met	His	Trp
	GTG	AAG	ATG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACA	TTT	ACC	AGT	TAC	AAT	ATG	CAC	TGG
		2517			2526			2535			2544			2553			2562		
			40		FR2				45			49	50			52	52A	53	54
	Val	Lys	Gln	Thr	Pro	Gly	Arg	Gly	Leu	Glu	Trp	Ile	Gly	Ala	Ile	Tyr	Pro	Gly	Asn
	GTA	AAA	CAG	ACA	CCT	GGT	CGG	GGC	CTG	GAA	TGG	ATT	GGA	GCT	ATT	TAT	CCC	GGA	AAT
		2574			2583			2592			2601			2610			2619		
		55			CDR2		60				65	66		FR3		70			
	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys
	GGT	GAT	ACT	TCC	TAC	AAT	CAG	AAG	TTC	AAA	GGC	AAG	GCC	ACA	TTG	ACT	GCA	GAC	AAA
		2631			2640			2649			2658			2667			2676		
			75				80		82	82A	82B	82C	83		85				
	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val
	TCC	TCC	AGC	ACA	GCC	TAC	ATG	CAG	CTC	AGC	AGC	CTG	ACA	TCT	GAG	GAC	TCT	GCG	GTC
		2688			2697			2706			2715			2724			2733		
						94	95		CDR3		100	100A	100B	100C	100D	101	102	103	
	Tyr	Tyr	Cys	Ala	Arg	Ser	Thr	Tyr	Tyr	Gly	Gly	Asp	Trp	Tyr	Phe	Asn	Val	Trp	Gly
	TAT	TAC	TGT	GCA	AGA	TCG	ACT	TAC	TAC	GGC	GGT	GAC	TGG	TAC	TTC	AAT	GTC	TGG	GGC
		2745			2754			2763			2772			2781			2790		

Figure 6

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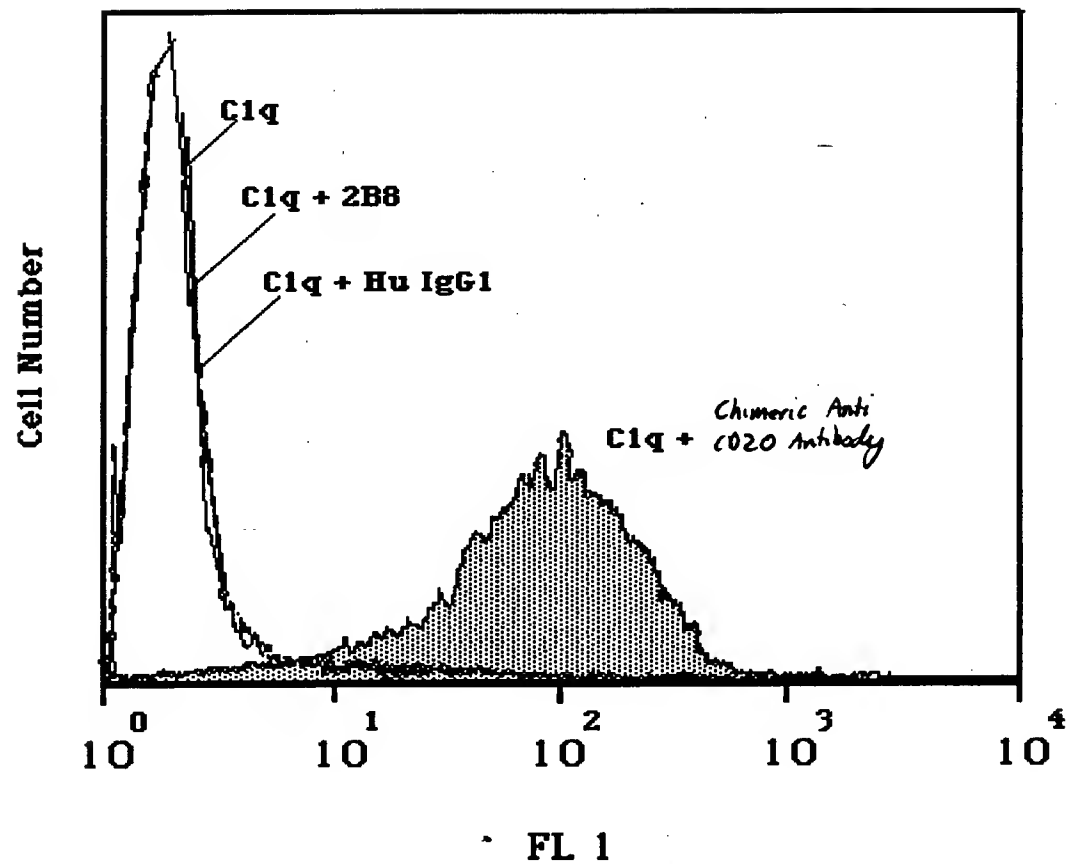
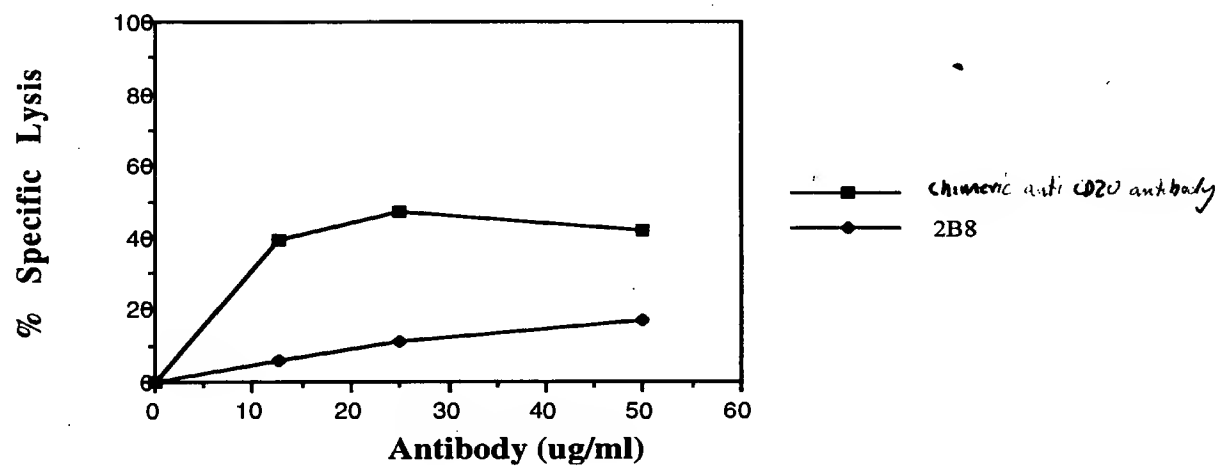
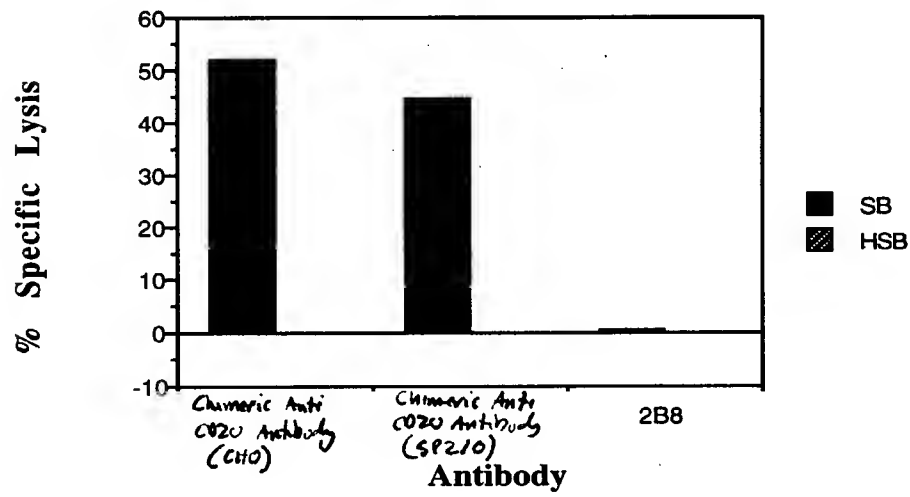


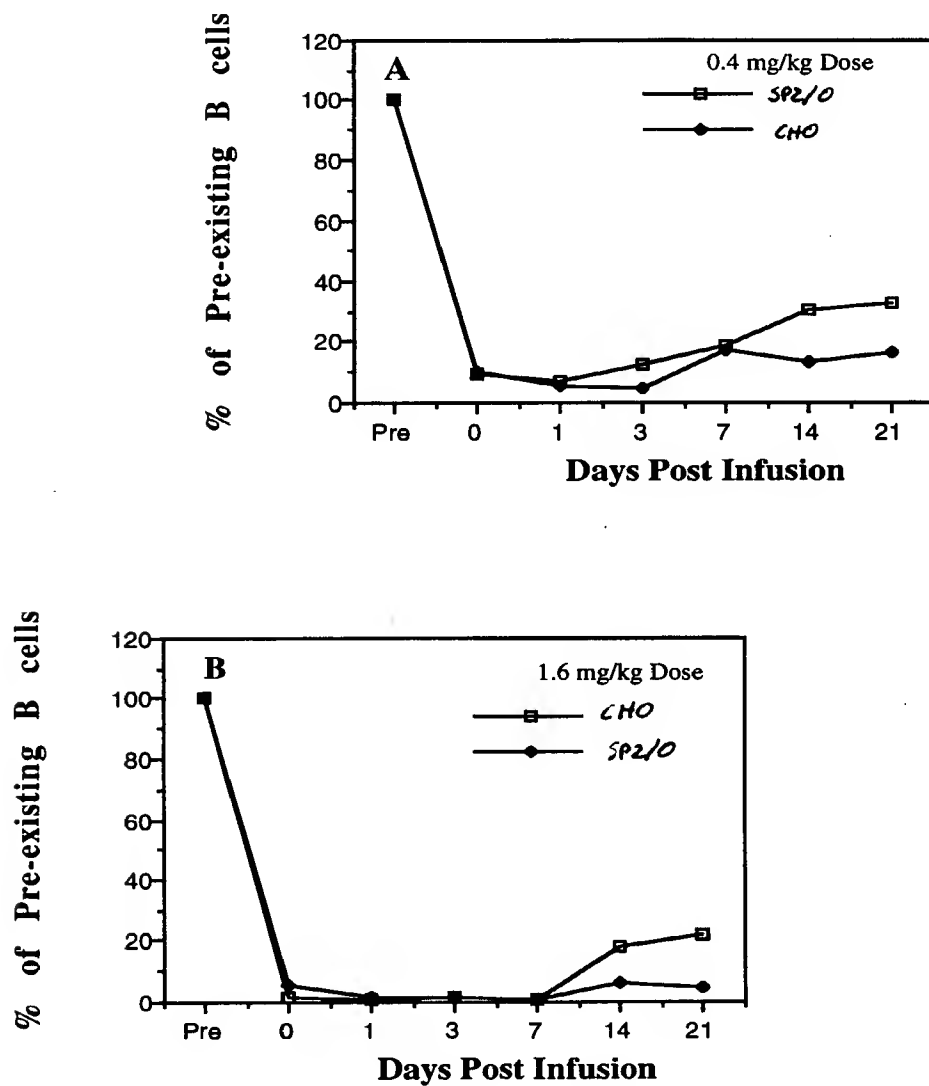
Figure 7

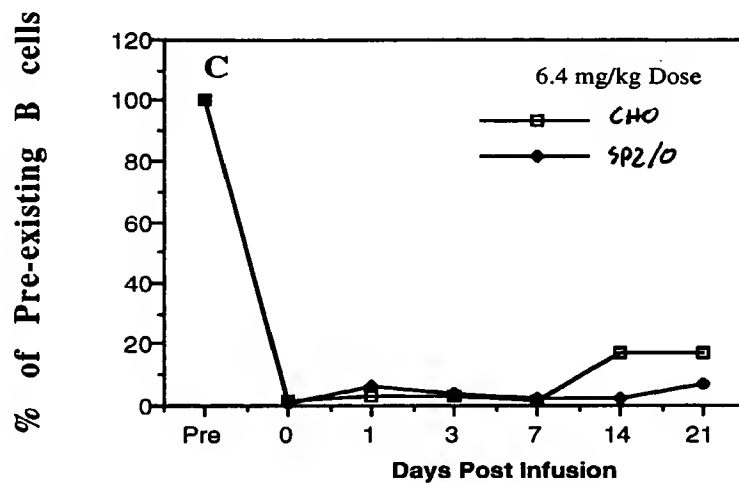
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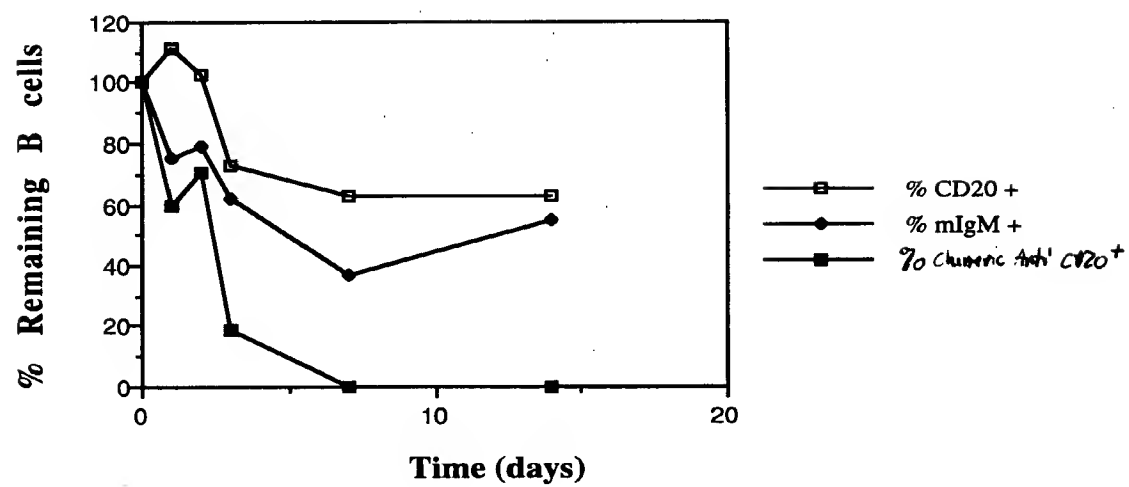




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